

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 14, 2003, 05:19:53 ; Search time 1.04494 Seconds

(without alignments)
827.996 Million cell updates/sec

Title: US-09-698-781-17

Perfect score: 44

Sequence: 1 TLFPVLLFL 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIRL3:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	245	2	S68691 neutrophil granule
2	36	81.8	161	2	E82044 fixa protein VC269
3	36	81.8	408	2	T39570 probable metal tra
4	35	79.5	222	2	G72297 conserved hypotet
5	35	79.5	227	2	F90624 ATP synthase F0 ch
6	35	79.5	361	2	D72384 conserved hypotet
7	35	79.5	543	2	E89839 hypotetrical prote
8	35	79.5	1325	2	T01037 hypotetrical prote
9	34	77.3	174	2	A70447 conserved hypotet
10	34	77.3	227	2	T11185 H+-transporting tw
11	34	77.3	237	2	H84035 hypotetrical prote
12	34	77.3	247	2	JE0307 membrane protein -
13	34	77.3	301	1	S12864 retinal isomerase
14	34	77.3	330	2	T34250 hypotetrical prote
15	34	77.3	356	2	G97072 uncharacterized con
16	34	77.3	405	2	B89976 hypotetrical prote
17	34	77.3	511	2	AG1912 hypotetrical prote
18	34	77.3	653	2	G82971 probable ferredoxi
19	34	77.3	741	2	T13086 NADH2 dehydrogenas
20	33	75.0	89	2	B86833 hypotetrical prote
21	33	75.0	303	2	AA3708 gamma-interferon-i
22	33	75.0	350	2	D64812 probable peroxidas
23	33	75.0	365	2	D71559 probable ABC ATPas
24	33	75.0	365	2	B81713 recf protein, prob
25	33	75.0	459	2	A99932 hypotetrical prote
26	33	75.0	483	2	G71523 probable arginine/
27	33	75.0	668	2	E96777 probable anion exc
28	33	75.0	744	2	T12705 NADH2 dehydrogenas
29	33	75.0	1007	2	PNO156 glutamate receptor

ALIGNMENTS

30	32	72.7	121	2	B64916 probable chaperone
31	32	72.7	121	2	B90917 probable chaperone
32	32	72.7	121	2	G85765 probable chaperone
33	32	72.7	195	2	A96998 CDP-diglyceride sy
34	32	72.7	231	2	AE0184 probable membrane
35	32	72.7	269	2	T38995 hypotetrical prote
36	32	72.7	331	2	A83377 conserved hypotet
37	32	72.7	333	2	C95368 hypotetrical prote
38	32	72.7	405	1	CBQFR ubiquinol-cytochro
39	32	72.7	461	2	S50864 avermectin-sensiti
40	32	72.7	495	2	T20754 hypotetrical prote
41	32	72.7	498	2	B80604 conserved hypotet
42	32	72.7	571	2	S00566 convicillin precurs
43	32	72.7	573	2	C86713 hypotetrical prote
44	32	72.7	601	2	T11190 NADH2 dehydrogenas
45	32	72.7	654	2	T29247 hypotetrical prote

RESULT 1

S68691 neutrophil granules matrix glycoprotein SGP28 precursor - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000

C:Accession: S68691; S74313; S68683

R:Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.

FEBS Lett. 380, 246-250, 1996

A:Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophil

A:Reference number: S68691; MUID:96186934; PMID:8601434

A:Accession: S68691

A:Molecule type: mRNA

A:Residues: 1-245 <KJE>

A:Cross-references: EMBL:X94323; NID:g1213612; PIDD:CA63984.1; PIDD:g1213613

A:Accession: S74313

A:Molecule type: Protein

A:Residues: 33-83;96-143;165-217;221-226 <KJD>

R:Kraetzschmar, J.; Haendler, B.; Eberspacher, U.; Roosterman, D.; Donner, P.; Schl.

Eur. J. Biochem. 236, 827-836, 1996

A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure

A:Reference number: S68681; MUID:96270732; PMID:865901

A:Accession: S68683

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-105; 'S', 107-245 <KRA>

A:Cross-references: EMBL:X95240; NID:g1262818; PIDD:CA64527.1; PIDD:g1262819

C:Genetics:

A:Gene: SGP28

C:Superfamily: cysteine-rich secretory protein 1

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <M

Query Match 100.0%; Score 44; DB 2; Length 245;

Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative

QY 1 TLFPVLLFL 9
DB 2 TLFPVLLFL 10

RESULT 2

E82044 fixa protein VC269 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: E82044

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Seller

L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: E82044
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-161 <HEI>
 A:Cross-references: GB:AE004335; GB:AE003852; NID:g9657289; PIDN:AAF95837.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
 C:Genetics:
 A:Gene: VC2696
 C:Superfamily: 1
 C:Superfamily: Escherichia coli hypothetical protein b4140

Query Match 81.8%; Score 36; DB 2; Length 161;
 Best Local Similarity 75.0%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 |||:||||
 DB 1 MFPILFL 8

RESULT 3
 T99570
 probable metal transporter - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T99570
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z21864
 A:Accession: T99570
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-408 <WOO>
 A:Cross-references: EMBL:AL035637; PIDN:CA838510.1; GSPDB:GN00067; SPDB:SPBC16D10.06
 A:Experimental source: strain 972h-; cosmid c16D10
 C:Genetics:
 A:Gene: SPDB:SPBC16D10.06
 A:Map position: 2

Query Match 81.8%; Score 36; DB 2; Length 408;
 Best Local Similarity 75.0%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLPVLLFL 8
 |||:||||
 DB 281 TLPVILIF 288

RESULT 4
 G72297
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: G72297
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: G72297
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-222 <ARN>
 A:Cross-references: GB:AE001768; GB:AE000512; NID:g4981619; PIDN:AAD36164.1; PID:g498163
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1087

Query Match 79.5%; Score 35; DB 2; Length 222;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLPVLLFL 9
 |||:||||
 DB 156 TLPVILFL 164

RESULT 5
 F90624
 ATP synthase F0 chain 6 [imported] - Casuarium casuarium mitochondrion
 C:Species: mitochondrion Casuarium casuarium
 C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 03-Aug-2001
 C:Accession: F90624
 R:Haddad, O.; Baker, A.J.
 Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001
 A:Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylo
 A:Reference number: A99613; MUID:21263106; PMID:11370967
 A:Accession: F90624
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-227 <KUR>
 A:Cross-references: GB:NC_002778; NID:g14141864; PIDN:NP_115355.1; GSPDB:GN00162
 C:Genetics:
 A:Gene: ATP6
 A:Genome: mitochondrion
 A:Genetic code: SGC1
 C:Superfamily: H+-transporting ATP synthase protein 6
 C:Keywords: mitochondrion

Query Match 79.5%; Score 35; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 8
 |||:||||
 DB 25 LFPVLLFL 31

RESULT 6
 D72384
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: D72384
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: D72384
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361 <ARN>
 A:Cross-references: GB:AE001718; GB:AE000512; NID:g4980881; PIDN:AAD35473.1; PID:g498
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM0388

Query Match 79.5%; Score 35; DB 2; Length 361;
 Best Local Similarity 75.0%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 |||:||||
 DB 25 LFPVLLFL 32

RESULT 7
 E89839
 hypothetical protein SA0639 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: E89839

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogudma, A.; Mitani, O.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuka, K.; Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: E89839
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-543 <KUR>
 A:Cross-references: GB:BA000018; PID:g13700575; PIDN:BA041872.1; GSPDB:GN00149
 A:Experimental source: strain N15
 C:Genetics:
 A:Gene: SA0639

Query Match 79.5%; Score 35; DB 2; Length 543;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 :||||:|
 DB 13 LFPVLMFL 20

RESULT 8

T01037
 Hypothetical protein YUP8H12R.20 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999
 C:Accession: T01037
 R:Phelios, A.; Vysotskaya, V.S.; Osborn, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwan, C.; Davis, R.W.
 Submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.
 A:Reference number: Z14227
 A:Accession: T01037
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1325 <THE>
 A:Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152582; GSPDB:GN00039; ATSP:YUP8H12R.20
 A:Map position: 1
 A:Introns: 70/; 130/3; 233/3; 384/3; 450/3; 470/1; 687/3; 740/3; 765/3; 868/3; 940/3; 1

Query Match 79.5%; Score 35; DB 2; Length 1325;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLFPVLLFL 9
 :||||:|
 DB 72 TLFPVLLFL 80

RESULT 9

A70447
 conserved hypothetical protein aq_1706 - Aquifex aeolicus

C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
 C:Accession: A70447
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A:Reference number: A70300; MUID:98198666; PMID:9537320
 A:Accession: A70447
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-174 <AOF>
 A:Cross-references: GB:AE000752; NID:g2984021; PIDN:AA07576.1; PID:g2984033; GB:AE00065
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: aq_1706

C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain
 Query Match 77.3%; Score 34; DB 2; Length 174;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 :||||:|
 DB 40 LFPVLLFL 47

RESULT 10

T11185

H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - *Smithornis sharpei* mtoc.
 C:Species: mitochondrion *Smithornis sharpei*
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
 C:Accession: T11185
 R:Minde, D.P.; Sorenson, M.D.; Dimcheff, D.E.
 Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998
 A:Title: Multiple independent origins of mitochondrial gene order in birds.
 A:Reference number: Z17242
 A:Accession: T11185
 A:Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-227 <MIN>
 A:Cross-references: EMBL:AF090340; NID:g4894488; PID:g4894494; PIDN:AD32519.1
 C:Genetics:
 A:Genome: mitochondrion
 A:Genetic code: SGC1
 C:Superfamily: H+-transporting ATP synthase protein 6
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 77.3%; Score 34; DB 2; Length 227;
 Best Local Similarity 75.0%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLFPVLLFL 8
 :||||:|
 DB 24 TLFPVLLFL 31

RESULT 11

H84035

Hypothetical protein BH3088 (imported) - *Bacillus halodurans* (strain C-125)
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H84035
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans*
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: H84035
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-237 <STO>
 A:Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06807.1; GSPDB:
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3088
 C:Superfamily: *Bacillus subtilis* hypothetical protein yoaT

Query Match 77.3%; Score 34; DB 2; Length 237;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 :||||:|
 DB 16 LFPVLLFL 23

DB 16 LFPVLLFL 23

RESULT 12

JF0307
 membrane protein - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
 R:Accession: JE0307
 R:Nakadell, T.; Kishimoto, T.; Kokura, K.; Ohkawa, N.; Makino, Y.; Muramatsu, M.; Tamura, DNA Res. 5, 315-317, 1998
 A:Title: Cloning of a novel rat gene, DB83, that encodes a putative membrane protein.
 A:Reference number: JE0307; MUID:99087491; PMID:9872456
 A:Accession: JE0307
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-247 <NAK>
 A:Cross-references: DDBJ:AB006135

Query Match 77.3%; Score 34; DB 2; Length 247;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LFPVLLFL 8
 Db 111 SIFPVLLFL 118

RESULT 13
 S12864
 retinal isomerase (EC 5.2.1.3) [validated] - Japanese flying squid
 N:Alternate names: retinochrome
 C:Species: Todarodes pacificus (Japanese flying squid)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 01-Sep-2000
 R:Accession: S12864; S39449
 R:Hara-Nishimura, I.; Matsunoto, T.; Morl, H.; Nishimura, M.; Hara, R.; Hara, T.
 FEBS Lett. 271, 106-110, 1990
 A:Title: Cloning and nucleotide sequence of cDNA for retinochrome, retinal photoisomerase
 A:Reference number: S12864; MUID:91032043; PMID:2226795
 A:Accession: S12864
 A:Molecule type: mRNA
 A:Residues: 1-301 <HAR>
 A:Cross-references: EMBL:X57143; NID:910776; PID:910777
 R:Hara-Nishimura, I.; Kondo, M.; Nishimura, M.; Hara, R.; Hara, T.
 FEBS Lett. 335, 94-98, 1993
 A:Title: Amino acid sequence surrounding the retinal-binding site in retinochrome of the
 A:Reference number: S39449; MUID:94063090; PMID:8243675
 A:Accession: S39449
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 274-277, 'X', 279-282 <HAR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: chromoprotein; cis-trans-isomerase; G protein-coupled receptor; glycoprotein
 F:1-301/Product: retinal isomerase #status experimental <MAT>
 F:19-43/Domain: transmembrane #status predicted <TM1>
 F:54-75/Domain: transmembrane #status predicted <TM2>
 F:95-120/Domain: transmembrane #status predicted <TM3>
 F:133-153/Domain: transmembrane #status predicted <TM4>
 F:181-208/Domain: transmembrane #status predicted <TM5>
 F:231-255/Domain: transmembrane #status predicted <TM6>
 F:265-288/Domain: transmembrane #status predicted <TM7>
 F:170/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:275/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 77.3%; Score 34; DB 1; Length 301;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LFPVLLFL 9
 Db 280 LFPVLLFL 287

RESULT 14
 T34250
 hypothetical protein F31D5.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34250

R:WILCOX, L.
 submitted to the EMBL Data Library, June 1995
 A:Description: The sequence of C. elegans cosmid F31D5.
 A:Reference number: 221494
 A:Accession: T34250
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-330 <WIL>
 A:Cross-references: EMBL:U28941; PIDN:AC71104.1; GSPDB:GN00020; CESP:F31D5.6
 C:Genetics:
 A:Gene: CESP:F31D5.6
 A:Map position: 2
 A:Insertions: 28/2; 46/1; 79/2; 158/1; 223/3; 281/2

Query Match 77.3%; Score 34; DB 2; Length 330;
 Best Local Similarity 77.8%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 LFPVLLFL 9
 Db 211 TTFPVALLFL 219

RESULT 15
 G97072
 uncharacterized conserved protein CAC1402 (similar to Icac of Staphylococcus and YHJR
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 R:Nolling, U.; Breton, G.; Omeletchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; I
 .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: G97072
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-356 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK79370.1; PID:G15024340; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1402

Query Match 77.3%; Score 34; DB 2; Length 356;
 Best Local Similarity 85.7%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LFPVLLFL 8
 Db 23 LFPVLLFL 29

Search completed: March 14, 2003, 05:41:35
 Job time : 4.04494 secs